

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/468,011A1812
#11
QE
9249
DATE: 09/16/97
TIME: 10:08:59

INPUT SET: S20361.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Soppet, Daniel R
6 Yi, Li
7 Rosen, Craig A
8 Ruben, Steven
9
10 (ii) TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
11 HLTG74
12
13 (iii) NUMBER OF SEQUENCES: 28
14
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
17 Stewart & Olstein
18 (B) STREET: 6 Becker Farm Road
19 (C) CITY: Roseland
20 (D) STATE: NJ
21 (E) COUNTRY: USA
22 (F) ZIP: 07068-1739
23
24 (v) COMPUTER READABLE FORM:
25 (A) MEDIUM TYPE: 3.5 INCH DISKETTE
26 (B) COMPUTER: IBM PS/2
27 (C) OPERATING SYSTEM: MS-DOS
28 (D) SOFTWARE: WORD PERFECT 5.1
29
30 (vi) CURRENT APPLICATION DATA:
31 (A) APPLICATION NUMBER: 08/468,011
32 (B) FILING DATE: 06-JUN-1995
33 (C) CLASSIFICATION:
34
35 (viii) ATTORNEY/AGENT INFORMATION:
36 (A) NAME: MULLINS, J.G.
37 (B) REGISTRATION NUMBER: 33,073
38 (C) REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
39
40 (ix) TELECOMMUNICATION INFORMATION:
41 (A) TELEPHONE: 201-994-1700
42 (B) TELEFAX: 201-994-1744
43
44
45 (2) INFORMATION FOR SEQ ID NO:1:
46

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47 (i) SEQUENCE CHARACTERISTICS:
48 (A) LENGTH: 2003 base pairs
49 (B) TYPE: nucleic acid
50 (C) STRANDEDNESS: single
51 (D) TOPOLOGY: linear
52
53 (ii) MOLECULE TYPE: cDNA
54
55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
56
57 GTTTGCTCTG GGCAGCCAAG TTGGCATATT GGAAGCTTTT TCCGGGCTCT GGAGGAGGGT 60
58
59 CCCTGCTTCT TCCTACAGCC GTTCCGGGC ATG GCC TGG CTG GGG GCG TCG CTC 113
60 Met Ala Trp Leu Gly Ala Ser Leu
61 1 5
62
63 CAC GTC TGG GGT TGG CTA ATG CTC GGC AGC TGC CTC CTG GCC AGA GCC 161
64 His Val Trp Gly Trp Leu Met Leu Gly Ser Cys Leu Leu Ala Arg Ala
65 10 15 20
66
67 CAG CTG GAT TCT GAT GGC ACC ATC ACT ATA GAG GAG CAG ATT GTC CTT 209
68 Gln Leu Asp Ser Asp Gly Thr Ile Thr Ile Glu Glu Gln Ile Val Leu
69 25 30 35 40
70
71 GTG CTG AAA GCG AAA GTA CAA TGT GAA CTC AAC ATC ACA GCT CAA CTC 257
72 Val Leu Lys Ala Lys Val Gln Cys Glu Leu Asn Ile Thr Ala Gln Leu
73 45 50 55
74
75 CAG GAG GGA GAA GGT AAT TGT TTC CCT GAA TGG GAT GGA CTC ATT TGT 305
76 Gln Glu Gly Glu Gly Asn Cys Phe Pro Glu Trp Asp Gly Leu Ile Cys
77 60 65 70
78
79 TGG CCC AGA GGA ACA GTG GGG AAA ATA TCG GCT GTT CCA TGC CCT CCT 353
80 Trp Pro Arg Gly Thr Val Gly Lys Ile Ser Ala Val Pro Cys Pro Pro
81 75 80 85
82
83 TAT ATT TAT GAC TTC AAC CAT AAA GGA GTT GCT TTC CGA CAC TGT AAC 401
84 Tyr Ile Tyr Asp Phe Asn His Lys Gly Val Ala Phe Arg His Cys Asn
85 90 95 100
86
87 CCC AAT GGA ACA TGG GAT TTT ATG CAC AGC TTA AAT AAA ACA TGG GCC 449
88 Pro Asn Gly Thr Trp Asp Phe Met His Ser Leu Asn Lys Thr Trp Ala
89 105 110 115 120
90
91 AAT TAT TCA GAC TGC CTT CGC TTT CTG CAG CCA GAT ATC AGC ATA GGA 497
92 Asn Tyr Ser Asp Cys Leu Arg Phe Leu Gln Pro Asp Ile Ser Ile Gly
93 125 130 135
94
95 AAG CAA GAA TTC TGT GAA CGC CTC TAT GTA ATG TAT ACC GTT GGC TAG 545
96 Lys Gln Glu Phe Cys Glu Arg Leu Tyr Val Met Tyr Thr Val Gly Tyr
97 140 145 150
98
99 TCC ATC TCT TTT GGT TCC TTG GCT GTG GCT ATT CTC ATC ATT GGT TAC 593

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100	Ser	Ile	Ser	Phe	Gly	Ser	Leu	Ala	Val	Ala	Ile	Leu	Ile	Ile	Gly	Tyr	
101			155					160					165				
102																	
103	TTC	AGA	CGA	TTG	CAT	TGC	ACT	AGG	AAC	TAT	ATC	CAC	ATG	CAC	TTA	TTT	641
104	Phe	Arg	Arg	Leu	His	Cys	Thr	Arg	Asn	Tyr	Ile	His	Met	His	Leu	Phe	
105			170				175					180					
106																	
107	GTG	TCT	TTC	ATG	CTG	AGA	GCT	ACA	AGC	ATC	TTT	GTC	AAA	GAC	AGA	GTA	689
108	Val	Ser	Phe	Met	Leu	Arg	Ala	Thr	Ser	Ile	Phe	Val	Lys	Asp	Arg	Val	
109	185					190					195					200	
110																	
111	GTC	CAT	GCT	CAC	ATA	GGA	GTA	AAG	GAG	CTG	GAG	TCC	CTA	ATA	ATG	CAG	737
112	Val	His	Ala	His	Ile	Gly	Val	Lys	Glu	Leu	Glu	Ser	Leu	Ile	Met	Gln	
113					205					210					215		
114																	
115	GAT	GAC	CCA	CAA	AAT	TCC	ATT	GAG	GCA	ACT	TCT	GTG	GAC	AAA	TCA	CAA	785
116	Asp	Asp	Pro	Gln	Asn	Ser	Ile	Glu	Ala	Thr	Ser	Val	Asp	Lys	Ser	Gln	
117				220				225					230				
118																	
119	TAT	ATC	GGG	TGC	AAG	ATT	GCT	GTT	GTG	ATG	TTT	ATT	TAC	TTC	CTG	GCT	833
120	Tyr	Ile	Gly	Cys	Lys	Ile	Ala	Val	Val	Met	Phe	Ile	Tyr	Phe	Leu	Ala	
121			235				240					245					
122																	
123	ACA	AAT	TAT	TAT	TGG	ATC	CTG	GTG	GAA	GGT	CTC	TAC	CTG	CAT	AAT	CTC	881
124	Thr	Asn	Tyr	Tyr	Trp	Ile	Leu	Val	Glu	Gly	Leu	Tyr	Leu	His	Asn	Leu	
125			250				255					260					
126																	
127	ATC	TTT	GTG	GCT	TTC	TTT	TCG	GAC	ACC	AAA	TAC	CTG	TGG	GGC	TTC	ATC	929
128	Ile	Phe	Val	Ala	Phe	Phe	Ser	Asp	Thr	Lys	Tyr	Leu	Trp	Gly	Phe	Ile	
129	265					270					275					280	
130																	
131	TTG	ATA	GGC	TGG	GGG	TTT	CCA	GCA	GCA	TTT	GTT	GCA	GCA	TGG	GCT	GTG	977
132	Leu	Ile	Gly	Trp	Gly	Phe	Pro	Ala	Ala	Phe	Val	Ala	Ala	Trp	Ala	Val	
133					285					290					295		
134																	
135	GCA	CGA	GCA	ACT	CTG	GCT	GAT	GCG	AGG	TGC	TGG	GAA	CTT	AGT	GCT	GGA	1025
136	Ala	Arg	Ala	Thr	Leu	Ala	Asp	Ala	Arg	Cys	Trp	Glu	Leu	Ser	Ala	Gly	
137				300					305					310			
138																	
139	GAC	ATC	AAG	TGG	ATT	TAT	CAA	GCA	CCG	ATC	TTA	GCA	GCT	ATT	GGG	CTG	1073
140	Asp	Ile	Lys	Trp	Ile	Tyr	Gln	Ala	Pro	Ile	Leu	Ala	Ala	Ile	Gly	Leu	
141			315					320					325				
142																	
143	AAT	TTT	ATT	CTG	TTT	CTG	AAT	ACG	GTT	AGA	GTT	CTA	GCT	ACC	AAA	ATC	1121
144	Asn	Phe	Ile	Leu	Phe	Leu	Asn	Thr	Val	Arg	Val	Leu	Ala	Thr	Lys	Ile	
145			330				335					340					
146																	
147	TGG	GAG	ACC	AAT	GCA	GTT	GGG	CAT	GAC	ACA	AGG	AAG	CAA	TAC	AGG	AAA	1169
148	Trp	Glu	Thr	Asn	Ala	Val	Gly	His	Asp	Thr	Arg	Lys	Gln	Tyr	Arg	Lys	
149	345					350					355					360	
150																	
151	CTG	GCC	AAA	TCG	ACA	CTG	GTC	CTG	GTC	CTA	GTC	TTT	GGA	GTG	CAT	TAC	1217
152	Leu	Ala	Lys	Ser	Thr	Leu	Val	Leu	Val	Leu	Val	Phe	Gly	Val	His	Tyr	

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	365	370	375	
153				
154				
155	ATC GTG TTC GTG TGC CTG CCT CAC TCC TTC ACT GGG CTC GGG TGG GAG			1265
156	Ile Val Phe Val Cys Leu Pro His Ser Phe Thr Gly Leu Gly Trp Glu			
157	380	385	390	
158				
159	ATC CGC ATG CAC TGT GAG CTC TTC TTC AAC TCC TTT CAG GGT TTC TTT			1313
160	Ile Arg Met His Cys Glu Leu Phe Phe Asn Ser Phe Gln Gly Phe Phe			
161	395	400	405	
162				
163	GTG TCT ATC ATC TAC TGC TAC TGC AAT GGA GAG GTT CAG GCA GAG GTG			1361
164	Val Ser Ile Ile Tyr Cys Tyr Cys Asn Gly Glu Val Gln Ala Glu Val			
165	410	415	420	
166				
167	AAG AAG ATG TGG AGT CGG TGG AAT CTC TCC GTG GAC TGG AAA AGG ACA			1409
168	Lys Lys Met Trp Ser Arg Trp Asn Leu Ser Val Asp Trp Lys Arg Thr			
169	425	430	435	440
170				
171	CCG CCA TGT GGC AGC CGC AGA TGC GGC TCA GTG CTC ACC ACC GTG ACG			1457
172	Pro Pro Cys Gly Ser Arg Arg Cys Gly Ser Val Leu Thr Thr Val Thr			
173	445	450	455	
174				
175	CAC AGC ACC AGC AGC CAG TCA CAG GTG GCG GCA GCA CAC GCA TGG TGC			1505
176	His Ser Thr Ser Ser Gln Ser Gln Val Ala Ala Ala His Ala Trp Cys			
177	460	465	470	
178				
179	TTA TCT CTG GCA AAG CTG CCA AGA TCG CCA GCA GAC AGC CTG ACA GCC			1553
180	Leu Ser Leu Ala Lys Leu Pro Arg Ser Pro Ala Asp Ser Leu Thr Ala			
181	475	480	485	
182				
183	ACA TCA CTT TAC CTG GCT ATG TCT GGA GTA ACT CAG AGC AGG ACT GCC			1601
184	Thr Ser Leu Tyr Leu Ala Met Ser Gly Val Thr Gln Ser Arg Thr Ala			
185	490	495	500	
186				
187	TCA CAC ACT CTC TCC ACG AGG AGC AAC AAG GAA GAT AGT GGG AGG CAG			1649
188	Ser His Thr Leu Ser Thr Arg Ser Asn Lys Glu Asp Ser Gly Arg Gln			
189	505	510	515	520
190				
191	AGA GAT GAT ATT CTA ATG GAG AAG CCT TCC AGG CCT ATG GAA TCT AAC			1697
192	Arg Asp Asp Ile Leu Met Glu Lys Pro Ser Arg Pro Met Glu Ser Asn			
193	525	530	535	
194				
195	CCA GAC ACT GAA GGA TGACAAGGAG AACTGAGGA TGTCTCTGA ATGGACATGT			1752
196	Pro Asp Thr Glu Gly			
197	540			
198				
199	GTGGCTGACT TTCATGGGC GGTCCAATGG CTGGTTGTGT GAGAGGGCTT GGCTGATACT			1812
200				
201	CCTATGCTTG AGCAAAAAGG CTGAAAATTC AGTTAAGGTG TTAATAATA ATAGTTTTTA			1872
202				
203	GGCTCCATGA ATTGCTCCT GTAAATACTA ACGACATGAA AATGCAAGTG TCAATGGAGT			1932
204				
205	AGTTTATTAC CTTCTATTGG CATCAAGTTT TCCTCTAAAT TAATGTATGG TATTTGCTCT			1992

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2003

206

207 GTGATTGTTC A

208

209

210 (2) INFORMATION FOR SEQ ID NO:2:

211

212 (i) SEQUENCE CHARACTERISTICS:

213 (A) LENGTH: 541 amino acids

214 (B) TYPE: amino acid

215 (D) TOPOLOGY: linear

216

217 (ii) MOLECULE TYPE: protein

218

219 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

220

221 Met Ala Trp Leu Gly Ala Ser Leu His Val Trp Gly Trp Leu Met Leu
222 5 10 15

223

224 Gly Ser Cys Leu Leu Ala Arg Ala Gln Leu Asp Ser Asp Gly Thr Ile
225 20 25 30

226

227 Thr Ile Glu Glu Gln Ile Val Leu Val Leu Lys Ala Lys Val Gln Cys
228 35 40 45

229

230 Glu Leu Asn Ile Thr Ala Gln Leu Gln Glu Gly Glu Gly Asn Cys Phe
231 50 55 60

232

233 Pro Glu Trp Asp Gly Leu Ile Cys Trp Pro Arg Gly Thr Val Gly Lys
234 65 70 75 80

235

236 Ile Ser Ala Val Pro Cys Pro Pro Tyr Ile Tyr Asp Phe Asn His Lys
237 85 90 95

238

239 Gly Val Ala Phe Arg His Cys Asn Pro Asn Gly Thr Trp Asp Phe Met
240 100 105 110

241

242 His Ser Leu Asn Lys Thr Trp Ala Asn Tyr Ser Asp Cys Leu Arg Phe
243 115 120 125

244

245 Leu Gln Pro Asp Ile Ser Ile Gly Lys Gln Glu Phe Cys Glu Arg Leu
246 130 135 140

247

248 Tyr Val Met Tyr Thr Val Gly Tyr Ser Ile Ser Phe Gly Ser Leu Ala
249 145 150 155 160

250

251 Val Ala Ile Leu Ile Ile Gly Tyr Phe Arg Arg Leu His Cys Thr Arg
252 165 170 175

253

254 Asn Tyr Ile His Met His Leu Phe Val Ser Phe Met Leu Arg Ala Thr
255 180 185 190

256

257 Ser Ile Phe Val Lys Asp Arg Val Val His Ala His Ile Gly Val Lys
258 195 200 205

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/468,011A

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Line

Error

Original Text